SEQUENCE LISTING

<110> Basi, Guriq
      Saldanha, Jose
      Yednock, Ted

<120> HUMANIZED ANTIBODIES THAT RECOGNIZE
      BETA AMYLOID PEPTIDE

<130> ELN-002

<140> US 10/010,942
<141> 2001-12-06

<150> US 60/251,892
<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 396
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(396)

<221> sig_peptide
<222> (1)...(60)

<400> 1
atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg   48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20   -15   -10   -5

gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg   96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
                1   5   10

gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc   144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
            15   20   25

ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg   192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
        30   35   40

cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac   240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45   50   55   60

tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt   288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                65   70   75

```
aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat   336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
            80              85              90

tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag   384
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95              100             105

ctg gaa atc aaa                                                   396
Leu Glu Ile Lys
    110
```

<210> 2
<211> 132
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(20)

<400> 2
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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20          -15              -10                          -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
             1               5               10
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15              20              25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
    30              35              40
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45              50              55                          60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
            65              70              75
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
            80              85              90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95              100             105
Leu Glu Ile Lys
    110
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<210> 3
<211> 414
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(414)

<221> sig_peptide
<222> (1)...(57)

<400> 3

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atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt    48
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
            -15                 -10                 -5

gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag    96
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            1               5                   10

cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc   144
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        15              20                  25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg   192
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30              35                  40                  45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca   240
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac   288
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                65                  70                  75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg   336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
            80                  85                  90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg   384
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
        95                  100                 105

ggc cag ggc acc act gtc aca gtc tcc tca                            414
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                 115
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<210> 4
<211> 138
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 4
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
            -15                 -10                 -5
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            1               5                   10
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        15              20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
30              35                  40                  45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
```

```
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
          65              70                  75
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
        80              85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95              100                 105
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110             115
```

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<210> 5
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20             -15             -10                 -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            1               5               10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15              20              25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
    30              35              40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45              50              55                  60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            65              70                  75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80              85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95              100                 105
Val Glu Ile Lys
    110
```

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<210> 6
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(13)

<400> 6
Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
            -10             -5                  1
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
    5               10              15
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
```

```
         20                        25                    30                        35
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
                40                        45                        50
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
            55                        60                        65
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
        70                        75                        80
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
    85                        90                        95
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100                       105                       110
```

<210> 7
<211> 100
<212> PRT
<213> Homo sapiens

<400> 7
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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1               5                   10                  15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20                        25                        30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                        40                        45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50                        55                        60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                        70                        75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                        90                        95
Leu Gln Thr Pro
            100
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<210> 8
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 3D6 heavy chain variable region

<221> SIGNAL
<222> (1)...(19)

<400> 8
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Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
                -15                   -10                       -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
             1               5                   10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                        20                        25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                        35                        40                        45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                        55                        60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
```

```
                     65 ·                    · 70                        75
    Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
            80                        85                    90
    Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
        95                       100                   105
    Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    110                   115
```

```
<210> 9
<211> 121
<212> PRT
<213> Homo sapiens
```

```
<400> 9
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1               5                  10                    15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            35                  40                  45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
        50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                      80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
            115                 120
```

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<210> 10
<211> 98
<212> PRT
<213> Homo sapiens
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```
<400> 10
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1               5                  10                    15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
        50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                      80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys
```

```
<210> 11
<211> 132
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```
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20              -15              -10                          -5
Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
                 1               5                   10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15              20                  25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
    30              35                  40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45              50                  55                      60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
        80                  85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105
Val Glu Ile Lys
    110


<210> 12
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 3D6 light chain variable region

<221> SIGNAL
<222> (1)...(19)

<400> 12
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
             -15              -10                  -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
             1               5                   10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        15              20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30              35                  40                      45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                65                  70                  75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
```

```
        95              .        100    .              105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110                  115


<210> 13
<211> 393
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(393)

<221> sig_peptide
<222> (1)...(57)

<400> 13
atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct    48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15                 -10                 -5

tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc    96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
                1               5                   10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att   144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
     15                  20                  25

ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca   192
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 30                  35                  40                  45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct   240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca   288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75

ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc   336
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
            80                  85                  90

ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg   384
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
     95                  100                 105

gag ctg gaa                                                        393
Glu Leu Glu
110


<210> 14
<211> 131
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<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 14
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Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
            -15                 -10                 -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
             1               5                 10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
    15              20                  25
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
            50                  55                  60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                  100                 105
Glu Leu Glu
110
```

<210> 15
<211> 426
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(426)

<221> sig_peptide
<222> (1)...(57)

<400> 15
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atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat    48
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
            -15                 -10                 -5

gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag    96
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            1               5                 10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg   144
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    15              20                  25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag   192
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
30                  35                  40                  45
```

```
ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat    240
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
            50                  55                  60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga    288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc    336
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
            80                  85                  90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct    384
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
        95                  100                 105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca            426
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120
```

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<210> 16
<211> 142
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 16
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
            -15                 -10                 -5
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
             1           5                  10
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    15                  20                  25
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
30                  35                  40                  45
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
            50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
            80                  85                  90
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
        95                  100                 105
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120


<210> 17
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
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<223> primer

<400> 17
tccgcaagct tgccgccacc atggacatgc gcgtgcccgc ccagctgctg ggcctgctga 60
tgctgtgggt gtccggctcc tccggctacg tggtgatgac ccagtccccc ctgtccctgc 120
ccgtgacccc cggcga   136

<210> 18
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
ctggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
cagcagggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
ggacaggggg g   131

<210> 19
<211> 146
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
acctgaactg gctgctgcag aagcccggcc agtcccccca gcgcctgatc tacctggtgt 60
ccaagctgga ctccggcgtg cccgaccgct tctccggctc cggctccggc accgacttca 120
ccctgaagat ctcccgcgtg gaggcc   146

<210> 20
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
aattctagga tccactcacg cttgatctcc accttggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg   142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
ctggggggac tggccg   16

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<210> 22
<211> 22 .
<212> DNA
<<213> Artificial Sequence

<220>
<223> primer

<400> 22
acctgaactg gctgctgcag aa                                        22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gcttttttctt gtggctattt 60
taaaaggtgt ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt                                            138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
gccgccggag cggatggagg ccacccactc caggcccttg ccggggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcaggagcc 120
gccgggctgc accag                                               135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
ctggagtggg tggcctccat ccgctccggc ggcggccgca cctactactc cgacaacgtg 60
aagggccgct tcaccatctc ccgcgacaac gccaagaact ccctgtacct gcagatgaac 120
tccctgcgcg ccgaggacac cg                                       142

<210> 26
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> primer
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<400> 26

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ctgcaaggat ccactcaccg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
gggagttcat ctgcaggtac aggg                                       144
```

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27

```
gccgccggag cggatg                                                16
```

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28

```
ctggagtggg tggcctccat                                            20
```

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29

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tccgcaagct tgccgccac                                             19
```

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30

```
aattctagga tccactcacg cttgatctc                                  29
```

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31 .
acagaaagct tgccgccacc atg   23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
ctgcaaggat ccactcaccg ga   22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> native ABeta peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1   5   10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
atggacatgc gcgtgcccgc ccagctgctg ggcctgctga tgctgtgggt gtccggctcc 60
tccggctacg tggtgatgac ccagtccccc ctgtccctgc ccgtgacccc cggcgagccc 120
gcctccatct cctgcaagtc ctcccagtcc ctgctggact ccgacggcaa gacctacctg 180
aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgcccga ccgcttctcc ggctccggct ccggcaccga cttcaccctg 300
aagatctccc gcgtggaggc cgaggacgtg ggcgtgtact actgctggca gggcacccac 360
ttccccccgca ccttcggcca gggcaccaag gtggagatca ag   402

<210> 35
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 2 VL

<400> 35
atggacatgc gcgtgcccgc ccagctgctg ggcctgctga tgctgtgggt gtccggctcc 60
tccggcgacg tggtgatgac ccagtccccc ctgtccctgc ccgtgacccc cggcgagccc 120
gcctccatct cctgcaagtc ctcccagtcc ctgctggact ccgacggcaa gacctacctg 180

```
aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgcccga ccgcttctcc ggctccggct ccggcaccga cttcaccctg 300
aagatctccc gcgtggaggc cgaggacgtg ggcgtgtact actgctggca gggcacccac 360
ttcccccgca ccttcggcca gggcaccaag gtggagatca ag                    402
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<210> 36
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VH

<400> 36
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gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg gcggctccct cgcctgtcc 120
tgcgccgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggccccc 180
ggcaagggcc tggagtgggt ggcctccatc cgctccggcg gcggccgcac ctactactcc 240
gacaacgtga agggccgctt caccatctcc cgcgacaacg ccaagaactc cctgtacctg 300
cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgcgtgcg ctacgaccac 360
tactccggct cctccgacta ctggggccag ggcaccctgg tgaccgtgtc ctcc       414
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<210> 37
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 2 VH

<400> 37
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tgcgccgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggccccc 180
ggcaagggcc tggagtgggt ggcctccatc cgctccggcg gcggccgcac ctactactcc 240
gacaacgtga agggccgctt caccatctcc cgcgacaact ccaagaacac cctgtacctg 300
cagatgaact ccctgcgcgc cgaggacacc gccgtgtact actgcgtgcg ctacgaccac 360
tactccggct cctccgacta ctggggccag ggcaccctgg tgaccgtgtc ctcc       414
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<210> 38
<211> 770
<212> PRT
<213> Homo sapiens

<400> 38
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Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1               5                   10                  15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35                  40                  45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95
```

```
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
        100                 105                 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
        115                 120                 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130                 135                 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145                 150                 155                 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165                 170                 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180                 185                 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
        195                 200                 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210                 215                 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225                 230                 235                 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245                 250                 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
        260                 265                 270
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
    275                 280                 285
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290                 295                 300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305                 310                 315                 320
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
            325                 330                 335
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
            340                 345                 350
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
        355                 360                 365
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
    370                 375                 380
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385                 390                 395                 400
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
                405                 410                 415
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
            420                 425                 430
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
        435                 440                 445
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
    450                 455                 460
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465                 470                 475                 480
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
            485                 490                 495
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
        500                 505                 510
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
    515                 520                 525
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
    530                 535                 540
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
```

```
         545                550               555                560
     Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
                     565               570               575
     Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
                 580               585               590
     Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
             595               600               605
     Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
         610               615               620
     Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
     625               630               635               640
     Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
                     645               650               655
     Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
                     660               665               670
     Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
                 675               680               685
     Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
         690               695               700
     Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
     705               710               715               720
     Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
                     725               730               735
     Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
                 740               745               750
     Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
                 755               760               765
     Gln Asn
     770
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<210> 39
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 39
actagtcgac atgaagttgc ctgttaggct gttggtgctg   40

<210> 40
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 40
actagtcgac atggagwcag acacactcct gytatgggt   39

<210> 41
<211> 40
<212> DNA
<213> Artificial Sequence

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<220>
<223> primer

<400> 41
actagtcgac atgagtgtgc tcactcaggt cctggsgttg                     40

<210> 42
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 42
actagtcgac atgaggrccc ctgctcagwt tyttggmwtc ttg                 43

<210> 43
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 43
actagtcgac atggatttwc aggtgcagat twtcagcttc                     40

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 44
actagtcgac atgaggtkcy ytgytsagyt yctgrgg                        37

<210> 45
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 45
actagtcgac atgggcwtca agatggagtc acakwyycwg g                   41

<210> 46
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<223> primer

<400> 46
actagtcgac atgtggggay ctktttycmm tttttcaatt g                    41

<210> 47
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
actagtcgac atggtrtccw casctcagtt ccttg                          35

<210> 48
<211> 37
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<220>
<223> primer

<400> 48
actagtcgac atgtatatat gtttgttgtc tatttct                        37

<210> 49
<211> 38
<212> DNA
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<220>
<223> primer

<400> 49
actagtcgac atggaagccc cagctcagct tctcttcc                       38

<210> 50
<211> 27
<212> DNA
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<220>
<223> primer

<400> 50
ggatcccggg tggatggtgg gaagatg                                   27

<210> 51
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer
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<400> 51
actagtcgac atgaaatgca gctgggtcat sttcttc 37

<210> 52
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 52
actagtcgac atgggatgga gctrtatcat sytctt 36

<210> 53
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 53
actagtcgac atgaagwtgt ggttaaactg ggttttt 37

<210> 54
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 54
actagtcgac atgractttg ggytcagctt grttt 35

<210> 55
<211> 40
<212> DNA
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<220>
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<400> 55
actagtcgac atggactcca ggctcaattt agttttcctt 40

<210> 56
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 56
actagtcgac atggctgtcy trgsgctrct cttctgc 37

<210> 57
<211> 36
<212> DNA
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<220>
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<400> 57
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<210> 58
<211> 33
<212> DNA
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<220>
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<400> 58
actagtcgac atgagagtgc tgattctttt gtg   33

<210> 59
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<400> 59
actagtcgac atggmttggg tgtggamctt gctattcctg   40

<210> 60
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<400> 60
actagtcgac atgggcagac ttacattctc attcctg   37

<210> 61
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<400> 61
actagtcgac atggattttg ggctgatttt ttttattg   38

<210> 62

<211> 37
<212> DNA.
<213> Artificial Sequence

<220>
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<400> 62
actagtcgac atgatggtgt taagtcttct gtacctg   37

<210> 63
<211> 27
<212> DNA
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<220>
<223> primer

<400> 63
ggatcccggg agtggataga ctgatgg   27